

GenCore version 4.5
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OM nucleic - nucleic search, using sw model.

Run on:

March 18, 2001, 07:16:03 ; Search time 885.31 Seconds

(without alignments)

2010.484 Million cell updates/sec

Title: US-09-199-129a-1.
 Perfect score: 254
 Sequence: 1 ggaatcttgaagcttaccta.....atgacnaaggcttcagaca 254
 Scoring table: IDENTITY_NUC
 Gapop 10.0 , Capext 1.0
 Searched: 7991742 seqs, 3503743858 residues
 #1 number of hits satisfying chosen parameters: 15983484
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : EST:
 1: gb_est1: *
 2: gb_est2: *
 3: gb_est3: *
 4: gb_est4: *
 5: gb_est5: *
 6: gb_est6: *
 7: gb_est7: *
 8: gb_est8: *
 9: gb_est9: *
 10: gb_est10: *
 11: gb_est11: *
 12: gb_est12: *
 13: gb_est13: *
 14: gb_est14: *
 15: gb_est15: *
 16: gb_est16: *
 17: gb_est17: *
 18: gb_est18: *
 19: gb_est19: *
 20: gb_est20: *
 21: gb_est21: *
 22: gb_est22: *
 23: gb_est23: *
 24: gb_est24: *
 25: gb_est25: *
 26: gb_est26: *
 27: gb_est27: *
 28: gb_est28: *
 29: gb_est29: *
 30: gb_est30: *
 31: gb_est31: *
 32: gb_est32: *
 33: gb_est33: *
 34: gb_est34: *
 35: gb_est35: *
 36: gb_est36: *
 37: gb_est37: *
 38: gb_est38: *
 39: gb_est39: *
 40: gb_est40: *
 41: em_estba: *
 42: em_lesthmu1: *

43: em_lesthmu1: *

44: em_esthmu2: *
 45: em_esthmu3: *
 46: em_esthmu4: *
 47: em_esthmu5: *
 48: em_esthmu6: *
 49: em_esthmu7: *
 50: em_esthmu8: *
 51: em_esthmu9: *
 52: em_esthmu10: *
 53: em_esthmu11: *
 54: em_esthmu12: *
 55: em_esthmu13: *
 56: em_esthmu14: *
 57: em_esthmu15: *
 58: em_esthmu16: *
 59: em_esthmu17: *
 60: em_esthmu18: *
 61: em_esthmu19: *
 62: em_esthmu20: *
 63: em_estin1: *
 64: em_estin2: *
 65: em_estin3: *
 66: em_estin4: *
 67: em_estov1: *
 68: em_estov2: *
 69: em_estp1: *
 70: em_estp2: *
 71: em_estp3: *
 72: em_estp4: *
 73: em_estp5: *
 74: em_estr1: *
 75: em_estr2: *
 76: em_estr3: *
 77: em_estr4: *
 78: em_estr5: *
 79: em_estr6: *
 80: em_estr7: *
 81: em_estr8: *
 82: em_estr9: *
 83: em_estr10: *
 84: em_estr11: *
 85: em_estr12: *
 86: em_estr13: *
 87: gb_est1: *
 88: gb_est42: *
 89: gb_est43: *
 90: gb_est44: *
 91: gb_est45: *
 92: gb_est13: *
 93: gb_est7: *
 94: gb_est48: *
 95: gb_est49: *
 96: gb_est50: *
 97: gb_est51: *
 98: gb_est52: *
 99: gb_est53: *
 100: gb_est54: *
 101: gb_est55: *
 102: gb_est56: *
 103: gb_est57: *
 104: gb_est67: *
 105: gb_est68: *
 106: gb_est69: *
 107: gb_est70: *
 108: gb_est71: *
 109: gb_est72: *
 110: gb_est73: *
 111: gb_est74: *
 112: em_esthmu21: *
 113: em_esthmu22: *
 114: em_esthmu23: *
 115: em_estom1: *
 116: em_estom2: *

117: em_estp16: *
 118: em_estp17: *
 119: em_estp18: *
 120: em_estr14: *
 121: em_estr15: *
 122: em_estr16: *
 123: em_estr17: *
 124: em_estr18: *
 125: em_estr19: *
 126: gb_est18: *
 127: gb_est59: *
 128: gb_est60: *

190: gb_gss25: *
 191: gb_gss26: *
 192: gb_gss27: *
 193: gb_gss28: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Length	DB	ID	Description
gb_est61: *	129:						
gb_est62: *	130:						
gb_est63: *	131:	1	127.6	50.2	477	28 AL369727	AL369727 MtBA32H11
gb_est64: *	132:	2	127.6	50.2	604	105 BE204104	BE204104 EST396780
gb_est65: *	133:	3	127.6	50.2	628	105 BE204201	BE204201 EST396870
gb_est66: *	134:	4	119.4	47.0	948	94 AW72203	AW72203 GA_Ba001
gb_est75: *	135:	5	110.4	43.5	463	108 BE42089	BE42089 EST324351
gb_est76: *	136:	6	110.4	43.5	468	137 BE921143	BE921143 EST424912
gb_est77: *	137:	7	108.8	42.8	263	39 AW041721	AW041721 EST384585
gb_est78: *	138:	8	108.8	42.8	608	108 BE449253	BE449253 EST35597108
gb_est79: *	139:	9	107.8	42.4	529	97 AW934135	AW934135 EST355979
gb_est80: *	140:	10	107.8	42.4	807	108 BE420773	BE420773 HWM002.D0
gb_est81: *	141:	11	104.6	41.2	714	105 BE193174	BE193174 HVSMEH008
gb_est82: *	142:	12	103.4	40.7	547	110 BE598903	BE598903 P1-83_A0
gb_est83: *	143:	13	102.8	40.5	290	28 AT002063	AT002063 AT001763
gb_est84: *	144:	14	102.8	40.5	411	28 AT001761	AT001761 AT001761
gb_est85: *	145:	15	99.6	39.2	564	93 BE624748	AW624748 EST322423
gb_est86: *	146:	16	99.2	39.1	646	106 BE320109	BE320109 NF025B04R
gb_est87: *	147:	17	99.2	39.1	699	92 AW584510	AW584510 N210564e
gb_gss1: *	148:	18	98.6	38.9	509	92 AW584529	AW584529 EST31503_P
gb_gss2: *	149:	19	96.4	38.0	417	26 A1898214	A1898214 EST267657
gb_gss3: *	150:	20	94.6	37.2	380	144 R65185	R65185 13689 Lambd
gb_gss4: *	151:	21	94.2	37.1	191	108 BE59125	BE59125 EST31447
em_gss1: *	152:	22	94	37.0	555	27 A193867	A193867 701515234
em_gss2: *	153:	23	82.4	32.4	474	29 AW084980	AW084980 AW084980
em_gss3: *	154:	24	80.6	31.7	494	29 AW54529	AW54529 PC03C03_P
em_gss4: *	155:	25	78.6	30.9	584	190 AG03012	AG03012 Oriza sat
gb_gss5: *	156:	26	77.2	30.4	337	111 BE622436	BE622436 ST85/ST85
gb_gss6: *	157:	27	77.2	30.4	344	87 AW226329	AW226329 ST81B02_P
gb_gss7: *	158:	28	77.2	30.4	351	90 AW431935	AW431935 ST78B07_P
gb_gss8: *	159:	29	77.2	30.4	380	87 AW226271	AW226271 ST80D009_P
gb_gss9: *	160:	30	77.2	30.4	389	39 AW05809	AW05809 ST56012_P
gb_gss10: *	161:	31	77.2	30.4	390	39 AW05655	AW05655 ST54C03_P
gb_gss11: *	162:	32	77.2	30.4	460	92 AW587778	AW587778 ST66G08_P
gb_gss12: *	163:	33	77.2	30.4	469	24 A1726703	A1726703 BNT6GH1637
gb_gss13: *	164:	34	77.2	30.4	573	39 AW042658	AW042658 ST22A07_P
gb_gss14: *	165:	35	77.2	30.4	601	39 AW043146	AW043146 ST22B08_P
gb_gss15: *	166:	36	77.2	30.4	601	39 AW043255	AW043255 ST31B10_P
gb_gss16: *	167:	37	77.2	30.4	700	93 AW668560	AW668560 GA_Ba001
gb_gss17: *	168:	38	77.2	30.4	775	38 AW010325	AW010325 ST04G01_P
gb_gss18: *	169:	39	77.2	30.4	889	94 AW731435	AW731435 GA_Ea003
gb_gss19: *	170:	40	77.2	30.4	973	94 AW731454	AW731454 GA_Ea003
gb_gss20: *	171:	41	76.2	30.0	109 BE559534	BE559534 M71H09STM	
gb_gss21: *	172:	42	76.2	30.0	250 AW551838	AW551838 AV551838	
gb_gss22: *	173:	43	76.2	30.0	384 37	37 AW042889	AW042889 ST26P06_P
gb_gss23: *	174:	44	76.2	30.0	549 39	39 AW50681	AW50681 AV550681
gb_gss24: *	175:	45	76.2	30.0	565 37	37 AW549801	AW549801 AV549801

ALIGNMENTS

RESULT	1
AL369727	AL369727 MtBA32H1F1 MtBA Medicago truncatula cDNA clone MtBA32H1 T3, mRNA DEFINITION sequence.
ACCESSION	AL369727
VERSION	AL369727.1
KEYWORDS	EST.
SOURCE	barrel medic.

			ORGANISM	Medicago truncatula
			Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;	Magnoliophyta; eudicots; core eudicots; Rosidae; eurosids I;
REFERENCE			Fabales; Fabaceae; Papillonoideae; Medicago.	Magnoliophyta; eudicots; core eudicots; Rosidae; eurosids I;
AUTHORS	1	(bases 1 to 477)	Journet, E.P., Crespeau, H., van-Tuinen, D., Gouzy, J., Jaillon, O., Niebel, A., Carreau, V., Chatagnier, O., Kahn, D., Gianinazzi-Pearson, V., and Gamas, P.	Fabales; Fabaceae; Papillonoideae; Medicago.
TITLE			Medicago truncatula ESTs from nitrogen-starved roots	
JOURNAL			CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email : mt-est@toulouse.inra.fr website : http://sequence.toulouse.inra.fr/mtruncatula.html).	
COMMENT			Contact: Genoscope Genoscope - Centre National de Séquençage BP 191 91006 Evry cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr	
FEATURES			Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire de Biologie Moléculaire des Relations Plantes-Microorganismes, CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email : mt-est@toulouse.inra.fr website : http://sequence.toulouse.inra.fr/mtruncatula.html).	
source			1. 477 '/cultivar="Jemalong" '/db_xref="taxon:3880" '/clone="MERA32H11" '/clone_lib="MTBA" '/tissue_type="root tips" '/dev_stage="harvested after 3 days of N-starvation" '/note="Vector: pBluescript PSK; Site_1: EcoRI; Site_2: XbaI; Plants were grown in an aeroponic chamber for 14 days on nitrogen-rich medium followed by 3 days on N-free medium. RNA was extracted from root tips (1-3 cm). cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into Uni-ZapXR vector from Stratagene and packaged using Gigapack Gold Packaging extracts. Plasmids containing cDNA inserts were mass-excised from phage stocks using Exsisi helper phage and propagated in SOLR cells. Clone ordering and sequencing was performed by the Centre National de Séquençage (Genoscope, Evry, France)."	
BASE COUNT	140	a 85 c 95 g 157 t	ORIGIN	
FEATURES			Query Match 50.2%; Score 127.6; DB 28; Length 477; Best Local Similarity 78.7%; Pred. No. 4e-29; Mismatches 148; Conservative 0; Indels 0; Gaps 0;	
source			67 ctactggncttttcccttcactcgacacttcattcgcgaggatttcttcgaaga 126 Db 98 CTCTTTCCTCTTAATACCTTCATTCTCATTCGAGATTTCCAGAGA 157 Qy 127 gatcgaagaaggatggaaaggcgcgtggatcancgatggaaaggatggaa 186 Db 158 CATCCAAGATGGAGAGTCGTTGGGTTATCTGATTTGAAAGAGGA 217 Qy 187 aacgggttaccttcaagcacacaggaaatggctggggatcccgatccaaatgtc 246 Db 218 AACGAAGTACCTTAACTGCGAAANTGGCTCGATGACCAAGGTA 277 Qy 247 ttccagca 254 Db 278 TTCAAGACA 285	
BASE COUNT	140	a 85 c 95 g 157 t	ORIGIN	
FEATURES			Query Match 50.2%; Score 127.6; DB 105; Length 604; Best Local Similarity 78.7%; Pred. No. 4.3e-29; Mismatches 148; Conservative 0; Indels 0; Gaps 0;	
source			67 ctactggncttttcccttcactcgacacttcattcgcgaggatttcttcgaaga 126 Db 13 CTCTTTCCTCTTAATACCTTCATTCTCATTCGAGATTTCCAGAGA 72 Qy 127 gatcgaagaaggatggaaaggcgcgtggatcancgatggaaaggatggaa 186 Db 73 CATCCAAGATGGAGAGTCGTTGGGTTATCTGATTTGAAAGAGGA 132 Qy 187 aacgggttaccttcaagcacacaggaaatggctggggatcccgatccaaatgtc 246 Db 133 AACGAAGTACCTTAACTGCGAAANTGGCTCGATGACCAAGGTA 192 Qy 247 ttccagaca 254 Db 193 TTCAAGACA 200	
RESULT	2		ORIGIN	
BE204104				
LOCUS	BE204104	604 bp mRNA	EST	05-SEP-2000
DEFINITION	EST96780	KV0 Medicago truncatula cDNA clone pkV0-14B21, mRNA sequence.		
ACCESSION	BE204104			
VERSION	BE204104.1	GR:8747387		
KEYWORDS		EST.		
RESULT	3		ORIGIN	
BE204201				
LOCUS	BE204201	628 bp mRNA	EST	05-SEP-2000
DEFINITION	EST96877	KV0 Medicago truncatula cDNA clone pkV0-14F14, mRNA sequence.		
ACCESSION	BE204201			
VERSION	BE204201.1	GI:8747485		
SOURCE			SOURCE	barrel medic.
ORGANISM			ORGANISM	Medicago truncatula
			Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;	
			Magnoliophyta; eudicots; core eudicots; Rosidae; eurosids I;	
REFERENCE			Fabales; Fabaceae; Papillonoideae; Medicago.	
AUTHORS	1	(bases 1 to 604)	VandenBosch, K., Endre, G., Hur, J., Moore, J., Beremand, P., Ellis, L., Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and Fraser, C.M.	
TITLE			ESTs from uninoculated seedling roots of Medicago truncatula	
JOURNAL			Unpublished (1999)	
COMMENT			Contact: Vandenbosch K	
			Department of Biology	
			Texas A&M University name:WIGA01RK	
			College Station, TX 77843-3258, USA	
			Tel: 409 845 7707	
			Fax: 409 845 2891	
			Email: katc@mail.bio.tamu.edu	
			Texas A&M University name:WIGA01RK	
			More information is available at:	
			http://achrysie.tamu.edu/medicago	
FEATURES			Seq primer: Skmed (CTA gAA CTA gtG gAT CC). location/Qualifiers	
source			1. .604 '/clone="Medicago truncatula" '/cultivar="genotype A17" '/db_xref="taxon:3880" '/clone="PKV0-14B21" '/clone.lib="KV0" '/tissue_type="Seedling roots" '/dev_stage="Immediately prior to inoculation with Sinorhizobium meliloti (0 hour)" '/lab_host="E.coli strain XLOR" '/note="Vector: pBluescript SK -; Site_1: EcoRI; Site_2: XbaI; cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the UniZap XR vector from Stratagene and packaged using Gigapack Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOR cells."	
BASE COUNT	140	a 85 c 95 g 157 t	ORIGIN	
FEATURES			Query Match 50.2%; Score 127.6; DB 105; Length 604; Best Local Similarity 78.7%; Pred. No. 4.3e-29; Mismatches 148; Conservative 0; Indels 0; Gaps 0;	
source			67 ctactggncttttcccttcactcgacacttcattcgcgaggatttcttcgaaga 126 Db 98 CTCTTTCCTCTTAATACCTTCATTCTCATTCGAGATTTCCAGAGA 157 Qy 127 gatcgaagaaggatggaaaggcgcgtggatcancgatggaaaggatggaa 186 Db 158 CATCCAAGATGGAGAGTCGTTGGGTTATCTGATTTGAAAGAGGA 217 Qy 187 aacgggttaccttcaagcacacaggaaatggctggggatcccgatccaaatgtc 246 Db 218 AACGAAGTACCTTAACTGCGAAANTGGCTCGATGACCAAGGTA 277 Qy 247 ttccagaca 254 Db 278 TTCAAGACA 200	
BASE COUNT	140	a 85 c 95 g 157 t	ORIGIN	
FEATURES			Query Match 50.2%; Score 127.6; DB 105; Length 604; Best Local Similarity 78.7%; Pred. No. 4.3e-29; Mismatches 148; Conservative 0; Indels 0; Gaps 0;	
source			67 ctactggncttttcccttcactcgacacttcattcgcgaggatttcttcgaaga 126 Db 13 CTCTTTCCTCTTAATACCTTCATTCTCATTCGAGATTTCCAGAGA 72 Qy 127 gatcgaagaaggatggaaaggcgcgtggatcancgatggaaaggatggaa 186 Db 73 CATCCAAGATGGAGAGTCGTTGGGTTATCTGATTTGAAAGAGGA 132 Qy 187 aacgggttaccttcaagcacacaggaaatggctggggatcccgatccaaatgtc 246 Db 133 AACGAAGTACCTTAACTGCGAAANTGGCTCGATGACCAAGGTA 192 Qy 247 ttccagaca 254 Db 193 TTCAAGACA 200	
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FEATURES			Query Match 50.2%; Score 127.6; DB 105; Length 604; Best Local Similarity 78.7%; Pred. No. 4.3e-29; Mismatches 148; Conservative 0; Indels 0; Gaps 0;	
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BASE COUNT	140	a 85 c 95 g 157 t	ORIGIN	
FEATURES			Query Match 50.2%; Score 127.6; DB 105; Length 604; Best Local Similarity 78.7%; Pred. No. 4.3e-29; Mismatches 148; Conservative 0; Indels 0; Gaps 0;	
source			67 ctactggncttttcccttcactcgacacttcattcgcgaggatttcttcgaaga 126 Db 98 CTCTTTCCTCTTAATACCTTCATTCTCATTCGAGATTTCCAGAGA 157 Qy 127 gatcgaagaaggatggaaaggcgcgtggatcancgatggaaaggatggaa 186 Db 158 CATCCAAGATGGAGAGTCGTTGGGTTATCTGATTTGAAAGAGGA 217 Qy 187 aacgggttaccttcaagcacacaggaaatggctggggatcccgatccaaatgtc 246 Db 218 AACGAAGTACCTTAACTGCGAAANTGGCTCGATGACCAAGGTA 277 Qy 247 ttccagaca 254 Db 278 TTCAAGACA 200	
BASE COUNT	140	a 85 c 95 g 157 t	ORIGIN	
FEATURES			Query Match 50.2%; Score 127.6; DB 105; Length 604; Best Local Similarity 78.7%; Pred. No. 4.3e-29; Mismatches 148; Conservative 0; Indels 0; Gaps 0;	
source			67 ctactggncttttcccttcactcgacacttcattcgcgaggatttcttcgaaga 126 Db 98 CTCTTTCCTCTTAATACCTTCATTCTCATTCGAGATTTCCAGAGA 157 Qy 127 gatcgaagaaggatggaaaggcgcgtggatcancgatggaaaggatggaa 186 Db 158 CATCCAAGATGGAGAGTCGTTGGGTTATCTGATTTGAAAGAGGA 217 Qy 187 aacgggttaccttcaagcacacaggaaatggctggggatcccgatccaaatgtc 246 Db 218 AACGAAGTACCTTAACTGCGAAANTGGCTCGATGACCAAGGTA 277 Qy 247 ttccagaca 254 Db 278 TTCAAGACA 200	
BASE COUNT	140	a 85 c 95 g 157 t	ORIGIN	
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source			67 ctactggncttttcccttcactcgacacttcattcgcgaggatttcttcgaaga 126 Db 98 CTCTTTCCTCTTAATACCTTCATTCTCATTCGAGATTTCCAGAGA 157 Qy 127 gatcgaagaaggatggaaaggcgcgtggatcancgatggaaaggatggaa 186 Db 158 CATCCAAGATGGAGAGTCGTTGGGTTATCTGATTTGAAAGAGGA 217 Qy 187 aacgggttaccttcaagcacacaggaaatggctggggatcccgatccaaatgtc 246 Db 218 AACGAAGTACCTTAACTGCGAAANTGGCTCGATGACCAAGGTA 277 Qy 247 ttccagaca 254 Db 278 TTCAAGACA 200	
BASE COUNT	140	a 85 c 95 g 157 t	ORIGIN	
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source			67 ctactggncttttcccttcactcgacacttcattcgcgaggatttcttcgaaga 126 Db 98 CTCTTTCCTCTTAATACCTTCATTCTCATTCGAGATTTCCAGAGA 157 Qy 127 gatcgaagaaggatggaaaggcgcgtggatcancgatggaaaggatggaa 186 Db 158 CATCCAAGATGGAGAGTCGTTGGGTTATCTGATTTGAAAGAGGA 217 Qy 187 aacgggttaccttcaagcacacaggaaatggctggggatcccgatccaaatgtc 246 Db 218 AACGAAGTACCTTAACTGCGAAANTGGCTCGATGACCAAGGTA 277 Qy 247 ttccagaca 254 Db 278 TTCAAGACA 200	
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BASE COUNT	140	a 85 c 95 g 157 t	ORIGIN	
FEATURES			Query Match 50.2%; Score 127.6; DB 105; Length 604; Best Local Similarity 78.7%; Pred. No. 4.3e-29; Mismatches 148; Conservative 0; Indels 0; Gaps 0;	
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BASE COUNT	140	a 85 c 95 g 157 t	ORIGIN	
FEATURES			Query Match 50.2%; Score 127.6; DB 105; Length 604; Best Local Similarity 78.7%; Pred. No. 4.3e-29; Mismatches 148; Conservative 0; Indels 0; Gaps 0;	
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BASE COUNT	140	a 85 c 95 g 157 t	ORIGIN	
FEATURES			Query Match 50.2%; Score 127.6; DB 105; Length 604; Best Local Similarity 78.7%; Pred. No. 4.3e-29; Mismatches 148; Conservative 0; Indels 0; Gaps 0;	
source			67 ctactggncttttcccttcactcgacacttcattcgcgaggatttcttcgaaga 126 Db 98 CT	

BASE COUNT	165 a	96 c	119 g	149 t	QY	160	tancggatggaaaggagtgaaaggaaaggggacttcagaacacqaggaaat	219
ORIGIN					Db	308	AATCCGATGGAAAGGAGCGAAGGAAACCGCAGGAAT	367
Query Match	42.4%				QY	160	tancggatggaaaggagtgaaaggaaaggggacttcagaacacqaggaaat	219
Best Local Similarity	75.6%				Db	368	ATCTGGGGATCTGATGACAAGGCATTCAACA	402
Matches	130; Conservative	0;	Mismatches	42; Indels 0; Gaps 0;	QY	220	99tctgggatcngatgacnaagggtttccagaca	254
OY	82	ttcnactctgcactttcatcgctgagattttccgaaaggatcgatgtat	141	RESULT 11	QY	220	99tctgggatcngatgacnaagggtttccagaca	254
Db	52	TTCATTATTACATCTCATTAATCTGAGATCTCTTGAAGACATTGATGATT	111	LOCUS BE193174	DEFINITION HVSMEH0080A07f Hordeum vulgare 5-45 DAP SPIKE EST library	EST	25-JUL-2000	
OY	142	ggaaaggccgtggggactccgtggaaaggatgtggaaaggaaaggggatctca	201	DEFINITION HVSMEH0080A009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEH0080A07f,	mRNA sequence.			
Db	112	GCGAGCAGATGGHGAAGCTGACTGGAAAGGAGTGAAGGAAAGCAGGTCCATTAA	171	ACCESSION BE193174	VERSION BE193174.1	GI:8705353		
OY	202	agcacacagcggaaatgtgtggatcengatgacnaagggtttccagac	253	KWONDS barley.	SOURCE	EST.		
Db	172	AGCATCACAGCTGGAAATGGCTGGTGTCTGTGATGATAAAGGTTTCAGAC	223	ORGANISM Hordeum vulgare	ORGANISM	Hordeum vulgare		
BLT	10			REFERENCE 1	REFERENCE 1	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophytidae; Liliopsida; Poales; Poaceae; Hordeum.		
LOCUS BE420773	BE420773	807 bp mRNA	EST	AUTHORS 1	AUTHORS 1	(bases 1 to 714)		
DEFINITION HVM02.D06	ITRC HVM Barley Leaf Library	Hordeum vulgare cDNA clone		WING, R., CLOSE, T., CLOUTIER, Y., ANDERSON, H., DALE, J., HENRY, D., KERNODLE, S., PALMER, M., RAMBO, T., SASKI, C., SCHWARTZBECK, J., SIMMONS, J., CHOI, D.W., MAIN, D. AND WOOD, T.				
ACCESSION BE420773	BE420773	mRNA sequence.		TITLE Development of a genetically and physically anchored EST resource for barley genomics				
VERSION BE420773.1	1	GI:9418616		JOURNAL Unpublished (2000)				
KEYWORDS EST				COMMENT Contact: Wing RA				
SOURCE barley.				CLEMSON UNIVERSITY GENOMICS INSTITUTE				
ORGANISM				100 JORDAN HALL, CLEMSON, SC 29634, USA				
Botany, Botanisches Institut der LMU				TEL: 864 656 7288				
Menzinger Str. 67, D-80638 München GERMANY				FAX: 864 656 4293				
Fax: 49 30 171683				EMAIL: rwing@clemson.edu				
Email: hermann@botanik.biologie.uni-muenchen.de				SEQ PRIMER: AATTAACCTCAATAAGG				
International Triticeae EST Cooperative (ITRC)				HVCDNA0009 (5 to 45 DAP)				
http://wheat.pw.usda.gov/genome.				HIGH QUALITY SEQUENCE START: 187				
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Scoring table:	IDENTITY_NUC	
	Gapop 10.0 , Gapext 1.0	
Searched:	28036 seqs, 80580151 residues	
1 number of hits satisfying chosen parameters:	561672	
Minimum DB seq length:	0	
Maximum DB seq length:	2000000000	
post-processing:	Minimum Match 0%	
	Maximum Match 100%	
Database :	Listing first 45 summaries	
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	4: /cgn2_6/ptodata/2/ina/PCUTS_COMB.seq:*	
	5: /cgn2_6/ptodata/2/ina/backfiles1.seq:*	
Pred. No. is the number of results predicted to have a score greater than or equal to the score of the best hit and is derived by analysis of the total score.		
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C 2	30.8	12.1 2518 3 US-09-433-699-3
C 3	29.2	11.5 3046 1 US-08-728-728-1
C 4	28.4	11.2 500 2 US-08-967-101-47
C 5	28.4	11.2 500 2 US-08-592-541-47
C 6	28.4	11.2 500 3 US-09-124-698-47
C 7	28	11.0 3303 1 US-08-081-610-3
C 8	28	11.0 6395 2 US-08-607-559-2
C 9	28	11.0 6395 3 US-09-239-741-1
C 10	28	11.0 6395 3 US-09-037-751-1
C 11	28	11.0 6425 3 US-09-259-741-3
C 12	28	11.0 6425 3 US-09-037-751-3
C 13	28	11.0 6439 3 US-09-239-741-2
C 14	28	11.0 6439 3 US-09-037-751-2
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C 16	28	11.0 6446 3 US-09-037-751-5
C 17	28	11.0 6475 3 US-09-259-741-4
C 18	28	11.0 6475 3 US-09-037-751-4
C 19	27.6	10.9 2012 2 US-08-449-933-3
C 20	27.6	10.9 8937 2 US-08-449-933-1
C 21	27.6	10.9 10706 1 US-08-411-389-1
C 22	27.4	10.8 43676 3 US-09-316-952-12
C 23	26.8	10.6 1211 3 US-08-956-182-23
C 24	26.8	10.6 1248 3 US-08-956-182-39
C 25	26.8	10.6 1266 3 US-08-916-182-27
C 26	26.8	10.6 1307 3 US-08-956-182-40
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	Sequence 14, Application US/08232463	
	PATENT NO. 5670367	
	GENERAL INFORMATION:	
	APPLICANT: DORNER, F.	
	APPLICANT: SCHEITLINGER, F.	
	APPLICANT: FAULKNER, F.G.	
	TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS	
	NUMBER OF SEQUENCES: 52	
	CORRESPONDENCE ADDRESS:	
	ADDRESSEE: Foley & Lardner	
	STREET: 1800 Diagonal Road, Suite 500	
	CITY: Alexandria	
	STATE: VA	
	ZIP: 22313-0299	
	COUNTRY: USA	
	COMPUTER READABLE FORM:	
	MEDIUM TYPE: Floppy disk	
	COMPUTER: IBM PC compatible	
	OPERATING SYSTEM: PC-DOS/MS-DOS	
	SOFTWARE: Patentin Release #1.0, version #1.25	
	CURRENT APPLICATION DATA:	
	APPLICATION NUMBER: US/08/232, 463	
	FILING DATE:	
	CLASSIFICATION: 435	
	PRIOR APPLICATION DATA:	
	APPLICATION NUMBER: US/07/935, 313	
	FILING DATE:	
	APPLICATION NUMBER: EP 91 114 300.6	
	FILING DATE: 20-AUG-1991	
	ATTORNEY/AGENT INFORMATION:	
	NAME: BENT, Stephen A.	
	REGISTRATION NUMBER: 29, 768	
	REFERENCE/DOCKET NUMBER: 30472/114 IMMU	
	TELECOMMUNICATION INFORMATION:	
	TELEPHONE: (703)836-9300	
	TELEFAX: (703)683-4109	
	TELEX: 899149	
	INFORMATION FOR SEQ ID NO: 14:	
	SEQUENCE CHARACTERISTICS:	
	LENGTH: 7218 base pairs	
	TYPE: nucleic acid	
	STRANDEDNESS: single	
	TOPOLOGY: linear	
	IMMEDIATE SOURCE:	
	CLONE: PTZ9PT-FLs	
	US-08-232-463-14	
	Query Match	13.2%; Score 33.6; DB 1; Length 7218;

Best Local Similarity 4.5%; Pred. No. 0.032; Matches 6; Conservative 85; Mismatches 43; Indels 0; Gaps 0;

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,725
FILING DATE:
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Baker, Jean C.
REGISTRATION NUMBER: 35,433
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5709
TELEFAX: (414) 271-3552
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3046 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

RESULT 2
S-09-433-699-3
Sequence 3, Application US/09433699B
Patent No. 6165786
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
TITLE OF INVENTION: ANTISENSE MODULATION OF NUCLEOLIN EXPRESSION
FILE REFERENCE: RTS-0109
CURRENT APPLICATION NUMBER: US/09/433,99B
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 3
LENGTH: 2518
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (112)..(2235)
SS-09-433-699-3

Query Match 12.1%; Score 30.8; DB 3; Length 2518;
Best Local Similarity 51.6%; Pred. No. 0.19; Matches 65; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

Query Match 11.5%; Score 30.8; DB 3; Length 2518;
Best Local Similarity 50.0%; Pred. No. 0.78; Matches 67; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

RESULT 4
S-08-726-755-1
Sequence 1, Application US/08/726725
Patient No. 5773290
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.

COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patientin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,101
FILING DATE: 10-Nov-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,725
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Jean C.
REGISTRATION NUMBER: 35,433
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5709
TELEFAX: (414) 271-3552
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3046 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

RESULT 1
S-08-726-725-1
Sequence 1, Application US/08/726725
Patient No. 5773290
GENERAL INFORMATION:
APPLICANT: Gould, Michael N.
APPLICANT: Chen, Kai-Shun
TITLE OF INVENTION: MAMMARY GLAND-SPECIFIC PROMOTERS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 411 East Wisconsin Avenue
CITY: Milwaukee
STATE: Wisconsin
COUNTRY: U.S.A.
ZIP: 53202-4497
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patientin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,101
FILING DATE: 10-Nov-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.

QY 192 ggtaacctcaaggcacacgaggaaatgtctq 225
 ; Sequence 3; Application US/09259741
 ; Patent No. 6033895
 ; GENERAL INFORMATION:
 ; APPLICANT: GARGER, STEPHEN
 ; APPLICANT: HOLTZ, R. BARRY
 ; APPLICANT: MCCULLOCH, MICHAEL
 ; APPLICANT: TURPEN, THOMAS
 ; TITLE OF INVENTION: A PROCESS FOR ISOLATING AND
 ; PURIFYING VIRUSES SOLUBLE PROTEINS AND PEPTIDES FROM PLANT SOURCES
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Howrey & Simon
 ; STREET: 1299 Pennsylvania Avenue N.W.
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FASTSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/259,741
 ; FILING DATE: February 25, 1999
 ; CLASSIFICATION:
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 09/037,751
 ; FILING DATE: March 10, 1998
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hallun, Albert P
 ; REGISTRATION NUMBER: 25,277
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-463-8109
 ; TELEFAX: 650-463-8400
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 6425 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: Genomic RNA
 ; US-09-259-741-3
 ;
 ; Query Match 11.0%; Score 28; DB 3; Length 6425;
 ; Best Local Similarity 46.8%; Pred. No. 3.1;
 ; Matches 44; Conservative 8; Mismatches 42; Indels 0; Gaps 0;
 ;
 ; RESULT 13
 ; OS-09-259-741-2
 ; Sequence 2; Application US/09259741
 ; Patent No. 6033895
 ; GENERAL INFORMATION:
 ; APPLICANT: GARGER, STEPHEN
 ; APPLICANT: HOLTZ, R. BARRY
 ; APPLICANT: MCCULLOCH, MICHAEL
 ; APPLICANT: TURPEN, THOMAS
 ; TITLE OF INVENTION: A PROCESS FOR ISOLATING AND
 ; PURIFYING VIRUSES SOLUBLE PROTEINS AND PEPTIDES FROM PLANT SOURCES
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ;
 ; Query Match 11.0%; Score 28; DB 3; Length 6425;
 ; Best Local Similarity 46.8%; Pred. No. 3.1;
 ; Matches 44; Conservative 8; Mismatches 42; Indels 0; Gaps 0;
 ;
 ; RESULT 14
 ; OS-09-259-741-3
 ; Sequence 3; Application US/09037751
 ; Patent No. 6037456
 ;
 ; RESULT 12
 ; OS-09-037-751-3
 ; sequence 3; Application US/09037751
 ; Patent No. 6037456
 ;
 ;

ADDRESSEE: Howrey & Simon
STREET: 1299 Pennsylvania Avenue N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/259,741
FILING DATE: February 25, 1999
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/037,751
FILING DATE: March 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P

REGISTRATION NUMBER: 25,277

REFERENCE/DOCKET NUMBER: 00801.0140.US01

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-463-8109
TELEFAX: 650-463-8400

TELEGRAM INFORMATION:
TELEPHONE: 650-463-8109

TELEX INFORMATION:
TELEPHONE: 650-463-8109

TELETYPE INFORMATION:
TELEPHONE: 650-463-8109

Query Match 11.0%; Score 28; DB 3; Length 6439;
Best Local Similarity 46.8%; Pred. No. 3.1; Mismatches 8; Indels 0; Gaps 0;
Matches 44; Conservative 42; Score 28; DB 3; Length 6439;
SEQUENCE CHARACTERISTICS:
LENGTH: 6439 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: Genomic RNA
US-09-259-741-2

RESULT 15
US-09-259-741-5
Sequence 5, Application US/09/259,741
Patent No. 6033695
GENERAL INFORMATION:
APPLICANT: GARGER, STEPHEN
APPLICANT: HOLTZ, R. BARRY
APPLICANT: MCCULLOCH, MICHAEL
APPLICANT: TURPEN, THOMAS
TITLE OF INVENTION: A PROCESS FOR ISOLATING AND PURIFYING VIRUSES SOLUBLE PROTEINS AND PEPTIDES FROM PLANT
TITLE OF INVENTION: PURIFYING VIRUSES SOLUBLE PROTEINS AND PEPTIDES FROM PLANT
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howrey & Simon
STREET: 1299 Pennsylvania Avenue N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/259,741
FILING DATE: February 25, 1999
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 09/037,751
FILING DATE: March 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/259,741
FILING DATE: February 25, 1999
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 09/037,751
FILING DATE: March 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P

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OM nucleic - nucleic search, using sw model

Run on: March 18, 2001, 07:17:18 : Search time 954.67 Seconds
(without alignments)
1361.631 Million cell updates/sec

Title: US-09-199-129a-1
Perfect score: 254
Sequence: 1 ggaatctgaagttaccta.....atgachaaaggtttcagaca 254
Scoring table: IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 1118133 seqs, 2558875100 residues
number of hits satisfying chosen parameters: 2236266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database	GenBml:
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	2: gb_ba2:*
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	4: gb_ov:*
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	7: gb_pl2:*
	8: gb_pr1:*
	9: gb_pr2:*
	10: gb_pr3:*
	11: gb_ro:*
	12: gb_sy:*
	13: gb_un:*
	14: em_fun:*
	15: em_hum1:*
	16: em_hum2:*
	17: em_in:*
	18: em_on:*
	19: em_or:*
	20: em_cv:*
	21: em_pat:*
	22: em_Ph:*
	23: em_Pl:*
	24: em_ro:*
	25: em_sts:*
	26: em_sy:*
	27: em_un:*
	28: em_vl:*
	29: gb_ba3:*
	30: gb_in1:*
	31: gb_in2:*
	32: gb_in3:*
	33: gb_Pl3:*
	34: gb_Pr4:*
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	39: em_htg3:*
	40: em_htg4:*
	41: em_htg5:*
	42: em_htg6:*
	43: em_htg7:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	95.6	37.6	1424	ATU66345
2	77	30.3	1564	BVWRNAC
3	76.4	30.1	1545	AF190454
4	76.2	30.0	1463	AF002057 Beta vulgaris
5	75.6	29.8	1547	AF066343 Arabidopsis
6	75.6	29.8	1593	AF052040 Barley
7	74.4	29.3	1558	AF283816 Nicotiana tabacum
8	74	29.1	1450	BLVCRH2A
9	74	29.1	1472	BLVCRH1A
10	74	29.1	1558	AB021259 Oryza sativa
11	72.6	28.6	1514	RCU74630
12	72.6	28.6	1543	CAPCRTC
13	72	28.3	89479	AF006932 Pinus taeda
14	71.6	28.2	1614	ZYMALPREC
15	70	27.6	1342	ZMCRTEGEN
16	70	27.6	7	ATU27698
17	69.4	27.3	1524	AF134733
18	66.8	26.3	1170	X85382 Nicotiana tabacum
19	65.6	25.8	78	D25481 Rice genome
20	65.2	25.7	1600	AF019376 Brassica
21	62.1	1363	32	U36937 Dictyostelia

JOURNAL	MEDLINE
Submitted (24-JUN-1996) Borisjuk N., Institut für Pflanzengenetik und Kulturpflanzenforschung Molekulare Genetik, AG Serologie Correnstr. 3 Gatersleben Germany D-06466 Location/Qualifiers	94339596 Location/Qualifiers
FEATURES source	/organism="Nicotiana plumbaginifolia"
5' UTR	/db_xref="taxon:4052"
gene	/dev_stake="somatic embryo"
CDS	/clone_libr="lambda zap"
5' UTR	1. .1558
gene	1. .22
CDS	23. .1273
gene	/gene="call1"
CDS	23. .1273
gene	/gene="call1"
gene	/function="ER Ca2+ binding protein"
codon_start	1
product	"calreticulin"
protein_id	"CAA95999.1"
db_xref	"GT:419088"
translation	"MATORRANPSSLHLITVFLSVLAVVSAEVFFESFDNGWESRWV
transliteration	"MATORRANPSSLHLITVFLSVLAVVSAEVFFESFDNGWESRWV
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FSVKEHQOKLDCGGGMLKLSGVQDGKQDPEYKPKLKVYQWLWQSGT	KQCPCEMDPSVHYTLTRPDNEKOTQSYHNDLIPKEIKPEKDPK
TNHILKEFPCETDOLITHYTIFLRDAYATISILDNEVKGSLISWDMLLPKTD	EWDKDEKIPDPEVKPGYDDJPKEVIDPDKPEMDDEGEWTATIP
PSAHRPEDDEKEFIDDPDKDPKPEYDDPEEITDPAKRPEDMDDEDEWTATIP	PNHQKKKPNYFOGKWPMTANDPFOODPYTIAFSIYKIGELWQVKSGTLPFDNL
NPEVKGPWPKKTIINPKQDPEYKPKLKVYQWLWQSGT	ITDAAIAKFLTEWKWIKDEKAADAEKKKEEDASKAGEDDDDDDEDDED
LFDNVICDPEYAKAISBTWQKQDAEKAAFEERAKREEEESKAAPADSAEEDD	KDRKAGSPADEKKDDKSDKDEKIDEL"
DADDSDDDDKSESKDDBAHDEL"	
s19-peptide	
mat_peptide	
3' UTR	
BASE COUNT	
ORIGIN	
Query Match	29.3%; Score 74.4; DB 33; Length 1558;
Best Local Similarity	67.1%; Pred. No. 5e-13; Matches 102; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
Matches	102; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
Qy	102 ttccgtgagatttttcgaaaggatggatggaaaggccgtgggtctca 161
Db	98 TCCGCTGAGCTCTTCGAGGAGTTAACGANGTGTTGAAAGCACGTGGCTGAA 157
BASE COUNT	483 a 327 c 380 g 368 t
ORIGIN	
Query Match	29.1%; Score 74; DB 7; Length 1450;
Best Local Similarity	67.3%; Pred. No. 6.6e-13; Matches 101; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
Matches	101; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
Qy	104 cgctgagatttttcgaaaggatggatggaaaggccgtgggtctca 163
Db	61 CGCCGACCTCTTCAGGAGATTCGAAGATGGCTGGGANAGCCGGTGGCTAACGTC 120
BASE COUNT	413 a 307 c 408 g 322 t
ORIGIN	
Query Match	29.1%; Score 74; DB 7; Length 1450;
Best Local Similarity	67.3%; Pred. No. 6.6e-13; Matches 101; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
Matches	101; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
Qy	104 cgctgagatttttcgaaaggatggatggaaaggccgtgggtctca 223
Db	121 TGATGGAAAGCACGAGACATGGCTGGATGGACCACATCINGAAATGGCA 180
BASE COUNT	413 a 307 c 408 g 322 t
ORIGIN	
RESULT	9
BLYCRH1A	BLYCRH1A 1472 bp mRNA
LOCUS	Hordeum vulgare calreticulin (CRH1) mRNA, partial cds.
DEFINITION	Hordeum vulgare calreticulin (CRH1) mRNA, partial cds.
VERSION	L27348.1 GI:439585
KEYWORDS	calcium-binding protein; calreticulin.
SOURCE	Hordeum vulgare (strain Morex) ovary cDNA to mRNA.
ORGANISM	Hordeum vulgare
REFERENCE	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Hordeum.
AUTHORS	1. (bases 1 to 1472)
TITLE	Identification and characterization of cDNA clones encoding plant calreticulin in barley
JOURNAL	Plant Cell 6, 835-843 (1994)
MEDLINE	94339696
FEATURES	Location/Qualifiers
source	1. .1472
gene	/organism="Hordeum vulgare"
CDS	/db_xref="taxon:4513"
gene	/tissue_type="ovary"
CDS	/map="1_M arm"
gene	3. .1238
CDS	/gene="CRH1"
<3> .>1246	

Query Match		Score	DB	Length	Best Local Similarity				Pred. No.				Matches			
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BASE COUNT	419	a	323	c	405	g	325	t	419	a	323	c	405	g	325	t
ORIGIN	453	a	330	c	437	g	337	t	453	a	330	c	437	g	337	t
RESULT 10																
DEFINITION	AB021259	1558	bp	mRNA	PLN		28-MAR-2000		REF ID:		RCU74330		RCU74630		1514	
ACCESSION	AB021259	Oryza sativa mRNA for calcium-binding protein, complete cds.		mRNA		PLN		29-SEP-1997		REF ID:		U74630		Ricinus communis calreticulin mRNA, complete cds.		
KEYWORDS	calcium-binding protein.	PLN		REF ID:		U74630.1		GI:1658196		REF ID:		U74630.1		GI:6682832		
SOURCE	Oryza sativa cDNA	ORGANISM		PLN		REF ID:		U74630.1		REF ID:		U74630.1		GI:6682832		
ORGANISM	Oryza sativa	PLN		REF ID:		U74630.1		REF ID:		U74630.1		REF ID:		U74630.1		
RESULT 11																
DEFINITION	AB021259.1	1514	bp	mRNA	PLN		29-SEP-1997		REF ID:		RCU74630		1514		bp	
ACCESSION	AB021259.1	GI:6682832		mRNA		PLN		29-SEP-1997		REF ID:		U74630		Ricinus communis calreticulin mRNA, complete cds.		
VERSION	224	REF ID:		U74630.1		REF ID:		GI:1658196		REF ID:		U74630.1		GI:6682832		
KEYWORDS	calcium-binding protein.	REF ID:		U74630.1		REF ID:		GI:1658196		REF ID:		U74630.1		GI:6682832		
SOURCE	Oryza sativa	ORGANISM		REF ID:		U74630.1		REF ID:		U74630.1		REF ID:		U74630.1		
ORGANISM	Oryza sativa	PLN		REF ID:		U74630.1		REF ID:		U74630.1		REF ID:		U74630.1		
RESULT 12																
DEFINITION	AB021259.2	1514	bp	mRNA	PLN		29-SEP-1997		REF ID:		RCU74630		1514		bp	
ACCESSION	AB021259.2	GI:6682832		mRNA		PLN		29-SEP-1997		REF ID:		U74630		Ricinus communis calreticulin mRNA, complete cds.		
VERSION	224	REF ID:		U74630.1		REF ID:		GI:1658196		REF ID:		U74630.1		GI:6682832		
KEYWORDS	calcium-binding protein.	REF ID:		U74630.1		REF ID:		GI:1658196		REF ID:		U74630.1		GI:6682832		
SOURCE	Oryza sativa	ORGANISM		REF ID:		U74630.1		REF ID:		U74630.1		REF ID:		U74630.1		
ORGANISM	Oryza sativa	PLN		<td data-kind="parent">REF ID:</td> <td data-kind="ghost"></td> <td data-cs="2" data-kind="parent">U74630.1</td> <td data-kind="ghost"></td> <td data-cs="2" data-kind="parent">REF ID:</td> <td data-kind="ghost"></td> <td data-cs="2" data-kind="parent">U74630.1</td> <td data-kind="ghost"></td> <td data-cs="2" data-kind="parent">REF ID:</td> <td data-kind="ghost"></td> <td data-cs="2" data-kind="parent">U74630.1</td> <td data-kind="ghost"></td>	REF ID:		U74630.1		REF ID:		U74630.1		REF ID:		U74630.1	
RESULT 13																
DEFINITION	AB021259.3	1514	bp	mRNA	PLN		29-SEP-1997		REF ID:		RCU74630		1514		bp	
ACCESSION	AB021259.3	GI:6682832		mRNA		PLN		29-SEP-1997		REF ID:		U74630		Ricinus communis calreticulin mRNA, complete cds.		
VERSION	224	REF ID:		U74630.1		REF ID:		GI:1658196		REF ID:		U74630.1		GI:6682832		
KEYWORDS	calcium-binding protein.	REF ID:		U74630.1		REF ID:		GI:1658196		REF ID:		U74630.1		GI:6682832		
SOURCE	Oryza sativa	ORGANISM		REF ID:		U74630.1		REF ID:		U74630.1		REF ID:		U74630.1		
ORGANISM	Oryza sativa	PLN		REF ID:		U74630.1		REF ID:		U74630.1		REF ID:		U74630.1		
RESULT 14																
DEFINITION	AB021259.4	1514	bp	mRNA	PLN		29-SEP-1997		REF ID:		RCU74630		1514		bp	
ACCESSION	AB021259.4	GI:6682832		mRNA		PLN		29-SEP-1997		REF ID:		U74630		Ricinus communis calreticulin mRNA, complete cds.		
VERSION	224	REF ID:		U74630.1		REF ID:		GI:1658196		REF ID:		U74630.1		GI:6682832		
KEYWORDS	calcium-binding protein.	REF ID:		U74630.1		REF ID:		GI:1658196		REF ID:		U74630.1		GI:6682832		
SOURCE	Oryza sativa	ORGANISM		REF ID:		U74630.1		REF ID:		U74630.1		REF ID:		U74630.1		
ORGANISM	Oryza sativa	PLN		REF ID:		U74630.1		REF ID:		U74630.1		REF ID:		U74630.1		
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ACCESSION	AB021259.5	GI:6682832		mRNA		PLN		29-SEP-1997		REF ID:		U74630		Ricinus communis calreticulin mRNA, complete cds.		
VERSION	224	REF ID:		U74630.1		REF ID:		GI:1658196		REF ID:		U74630.1		GI:6682832		
KEYWORDS	calcium-binding protein.	REF ID:		U74630.1		REF ID:		GI:1658196		REF ID:		U74630.1		GI:6682832		
SOURCE	Oryza sativa	ORGANISM		REF ID:		U74630.1		REF ID:		U74630.1		REF ID:		U74630.1		
ORGANISM	Oryza sativa	PLN		REF ID:		U74630.1		REF ID:		U74630.1		REF ID:		U74630.1		
RESULT 16																
DEFINITION	AB021259.6	1514	bp	mRNA	PLN		29-SEP-1997		REF ID:		RCU74630		1514		bp	
ACCESSION	AB021259.6	GI:6682832		mRNA		PLN		29-SEP-1997		REF ID:		U74630		Ricinus communis calreticulin mRNA, complete cds.		
VERSION	224	REF ID:		U74630.1		REF ID:		GI:1658196		REF ID:		U74630.1		GI:6682832		
KEYWORDS	calcium-binding protein.	REF ID:		U74630.1		REF ID:		GI:1658196		REF ID:		U74630.1		GI:6682832		
SOURCE	Oryza sativa	ORGANISM		REF ID:		U74630.1		REF ID:		U74630.1		REF ID:		U74630.1		
ORGANISM	Oryza sativa	PLN		REF ID:		U74630.1		REF ID:		U74630.1		REF ID:		U74630.1		
RESULT 17																
DEFINITION	AB021259.7	1514	bp	mRNA	PLN		29-SEP-1997		REF ID:		RCU74630		1514		bp	
ACCESSION	AB021259.7	GI:6682832		mRNA		PLN		29-SEP-1997		REF ID:		U74630		Ricinus communis calreticulin mRNA, complete cds.		
VERSION	224	REF ID:		U74630.1		REF ID:		GI:1658196		REF ID:		U74630.1		GI:6682832		
KEYWORDS	calcium-binding protein.	REF ID:		U74630.1		REF ID:		GI:1658196		REF ID:		U74630.1		GI:6682832		
SOURCE	Oryza sativa	ORGANISM		REF ID:		U74630.1		REF ID:		U74630.1		REF ID:		U74630.1		
ORGANISM	Oryza sativa	PLN		REF ID:		U74630.1		REF ID:		U74630.1		REF ID:		U74630.1		
RESULT 18																
DEFINITION	AB021259.8	1514	bp	mRNA	PLN		29-SEP-1997		REF ID:		RCU74630		1514		bp	
ACCESSION	AB021259.8	GI:6682832		mRNA		PLN		29-SEP-1997		REF ID:		U74630		Ricinus communis calreticulin mRNA, complete cds.		
VERSION	224	REF ID:														


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QSILDTLAASPVIDQMAVAGK1UNIEGFTQADNIRQHTVPHOLRQEEALTVQAR
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Mon Mar 19 12:20:51 2001

us-09-199-129a-1.rge

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Db 194 TGGAGAAGGATGAGAACATGGCGTGAATGGACACACCTGGAAATGGATGGA 253
QY 228 gatccengatgacnaagg tcttcagac 253
||| ||| ||| ||| ||| ||| |||
Db 254 GATCCGAGGACAAGGTATTCAAC 279

Search completed: March 18, 2001, 07:53:46
Job time: 2188 sec

GenCore version 4.5
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Ed.

OM nucleic - nucleic search, using sw model
Run on: March 18, 2001, 07:19:53 : Search time 73.44 Seconds

Title: US-09-199-129A-1
 Perfect score: 254
 Sequence: tggaaatcgaaggtaacctta.....atgacnaaaggcttcagaca 254
 Scoring table: IDENTITY.NUC
 Gapp 10.0 , Gapext 1.0
 Searched: 480022 seqs, 187831343 residues
 Minimum DB seq length: 0
 Maximum DB seq length: 200000000
 Post processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

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Pred. No. 19 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query	Match Length	DB	ID
1	30.8	12.1	2518	20	V11745
2	30.2	11.9	10942	20	X17142
3	29.8	11.7	1230025	20	X91990
4	29.4	11.6	1361	20	X16671
5	29.2	11.5	3046	19	X22074
6	29	11.4	401	14	Q68005
7	28.6	11.3	250	20	X10841
8	28.6	11.3	323	20	X0452
9	28.6	11.3	2168	20	X52271
10	28.4	11.2	251	20	V0169
11	28.4	11.2	2082	15	Q55799
12	28.4	11.2	2382	12	Q0238

Description

- Human V3 loop HIV
- Human V3 loop HIV
- Nucleotide sequence
- G-protein coupled
- Rattus norvegicus
- Human brain Express
- Human secreted protein
- Human secreted protein
- Protein PRO330 CDN
- EST clone DF706
- Sequence comprising
- Encodes membrane e

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

us-09-199-129a-1.rng

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FT intron /**tag= 2226_3438
FT exon /number= 2
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FT exon /tag= f
FT intron /number= 3
FT intron /**tag= 3917_4586
FT exon /number= 3
FT exon /tag= h
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FT intron /tag= q
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FT exon /tag= v
FT exon /tag= w
FT exon /tag= x
FT exon /tag= y
FT exon /tag= z

```


CC and portions may have therapeutic applications in wound healing and tissue repair; PRO317 can be used for treating problems of the kidney, uterus, endometrium, blood vessels, or related tissue, e.g. in the heart of genital tract.

XX

Sequence 2168 BP; 538 A; 523 C; 601 G; 506 T; 0 other;

Db 128 gtctctggccagagcag 144

LT 10

v90169/C ID v90169 standard; cDNA; 251 BP.

AC

v90169;

XX

DT 15-FEB-1999 (first entry)

XX

DE EST clone DF706.

XX

OS Homo sapiens.

XX

KW Human; secreted protein; expressed sequence tag; EST; haemopoiesis; tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic; receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour; gene therapy; ss.

XX

KW gene therapy; ss.

XX

KW Homo sapiens.

XX

PN WO9845436-A2.

XX

PD 15-OCT-1998.

XX

PP 10-APR-1998; 98WO-US06955.

XX

PR 10-APR-1997; 97US-0838821.

XX

PA (GEMY) GENETICS INST INC.

XX

X Agostino MJ, Jacobs K, Lavaltrie ER, McCoy JM, Merberg D;

XX

DR Racie LA, Spaulding V, Tracy M;

XX

WPI; 1999-070077/06.

XX

PT New polyucleotides encoding human secreted proteins - derived from e.g. human blood, kidney, foetal lung, Placenta, testes, brain, ovary, pituitary, retina and colon cDNA libraries.

XX

PS Claim 1; Page 453; 618pp; English.

XX

CC The present sequence represents a human expressed sequence tag (EST).

CC arc predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haemopoiesis regulating activity, tissue growth activity, activin/inhibin activity, chemotactic/chemokinetic activity and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The polyucleotide may also be useful for gene therapy.

XX

Sequence 251 BP; 35 A; 100 C; 18 G; 98 T; 0 other;

Query Match Similarity 11.3%; Score 28.4; DB 20; Length 251; Best Local Similarity 50.0%; Pred. No. 1; Mismatches 65; Indels 0; Gaps 0; Matches 65; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 137 tggatcgasagcgcgttgcgtttcccgatggaaaggatggagaaaaacgggtac 196
Db 68 tgccagaacccgacggatgtgcataaccctggacaggatggagacggcggaaag 127

QY 197 cttagacacacacag 213
Db 128 gtctctggccagagcag 144

RESULT 11
ID 055789 standard; DNA; 2082 BP.
XX
AC 055789;
XX
DR 20-JUL-1994 (first entry)
XX
DE Sequence comprising membrane exon of Ig membrane anchoring peptide.
XX
KW Isoform; peptide; anchoring protein; membrane spanning protein; transmembrane domain; immunoglobulin; B cell; immune system; ss.
XX
OS Homo sapiens.
XX
FH Key
FT exon
FT /note= "Membrane exon of human alpha-1 membrane anchoring peptide. (Isoform 1)."
FT exon
FT /note= "Membrane exon of human alpha-1 membrane anchoring peptide. (Isoform 2)."
FT misc_difference 1615..1617 /tag= C
FT /note= "CRC encodes Valine."
XX
PN US5281699-A.
XX
PD 25-JAN-1994.
XX
PF 01-JUN-1990; 90US-0531787.
XX
PR 01-JUN-1990; 90US-0531787.
XX
PA (TANO) TANOX BIOSYSTEMS INC.
XX
PI Chang TW;
XX
DR WPI; 1994-042862/05.
XX
PT P-PSDB; R47922, R53709.

XX
PT New peptide(s) representing extracellular immunoglobulin gamma epitope(s) - for generating isotype specific antibodies, used to kill B cells involved in leukaemia and lymphoma
XX
PS Disclosure; Figure 6; 22pp; English.
XX
CC The heavy chains of immunoglobulins contain membrane anchoring peptides which span the cell membrane lipid bilayer, fixing the associated immunoglobulin to the cell membrane surface. The extracellular portions of these peptides are unique for different isotypes, but tend to be similar among different subclasses of a

CC

particular isotype. The extracellular segment forms an epitope unique to the B cells which produce each isotype. These membrane bound immunoglobulin isotype-specific extracellular epitopes are not present on the secreted, soluble form of the immunoglobulins.

XX Sequence 2082 BP; 491 A; 459 C; 712 G; 399 T; 21 other;

Query Match 11.2%; Score 28.4; DB 15; Length 2082;
Best Local Similarity 55.2%; Pred. No. 4.7;
Matches 53; Conservative 0; Mismatches 43; Indels 0; Gaps 0;
Db 132 gaaatgatgtggaaaggcccgctgtgtcancattgtggaaaggatcaagaaacg 191
752 gatggaggatgtggggatggaggatggatgtggatgggggtgaatggaggatg 811
Qy 192 ggtccttcagaacacacgcggaaaatgttcgg 227
Db 812 ggtagactgacggaggattggatactgggtgg 847

R_ LT 12

ID Q10238 standard; cDNA; 2382 BP.
XX AC Q10238;

XX DT 22-MAR-1991 (first entry)

DE Encodes membrane exon of IgA membrane anchoring peptide.

XX alpha.mb/ec; immunoglobulin A; IgA; allergy; membrane-anchoring; peptide; ss.

XX OS Homo sapiens.

FH Key Location/Qualifiers
exon 1741..1956

FT /*tag= a
FT /product= alpha.mb/ec
FT /note= "membrane-anchoring peptide"
FT polyA_signal 2361..2366

FT /*tag= b
W09015614-A.

FT XX PD 27-DEC-1990.

FT XX PR 21-JUN-1990; 90WQ-US03532.

PR 22-DEC-1989; 89US-0455080.

PR 21-JUN-1989; 89US-0369479.

XX PA (TANO-) TANOX BIOSYST INC.

XX PI Chang TW; Chang NY;
XX DR WPI; 1991-022051/03.

DR R-PSDB; R10202.

XX PT Antibody prep. which binds specifically to immunoglobulin A -
PT bound to B cells, but not secreted form, to enhance IgA prodn.
XX and protect against allergy and infection

PS Disclosure; Fig 1; 54pp; English.
XX Clones containing alpha 1 heavy chain gene segments were identified from a human genomic library subcloned and sequenced. A segment of 194 nucleotides was determined to be the membrane exon of the alpha 1 gene. To confirm this, total RNA was isolated from a human mIgA-expressing cell line DAKIK and cDNA prepared from it. Positive clones were sequenced and two species of human membrane-bound alpha 1 mRNA were found, resulting from two different splice sites and

CC encoding two isoforms. Isoform 2 is the one corresponding to R10202; CC isoform 1 lacks the first 6 N-terminal amino acids. The nucleotide sequence of human alpha 1 is homologous to that of murine alpha.

XX Sequence 2382 BP; 555 A; 549 C; 809 G; 469 T; 0 other;

Query Match 11.2%; Score 28.4; DB 12; Length 2382;
Best Local Similarity 55.2%; Pred. No. 5;
Matches 53; Conservative 0; Mismatches 43; Indels 0; Gaps 0;
Db 132 gaaatgatgtggaaaggcccgctgtgtcancattgtggaaaggatcaagaaacg 191
752 gatggaggatgtggggatggaggatggatgtggatgggggtgaatggaggatg 811
Qy 192 ggtagactgacggaggattggatactgggtgg 227
Db 812 ggtagactgacggaggattggaggatactgggtgg 847

RESULT 13

ID X91788/C
XX ID x91788 standard; DNA; 3525 BP.
XX AC X91788;

XX DT 25-AUG-1999 (first entry)

DE Porphrymonas gingivalis protein PG encoding DNA.

XX Porphyromonas gingivalis; PG; periodontal disease; gingivitis;

XX vaccine; antigenic; ds.

OS Porphrymonas gingivalis.

XX PN W09029870-A1.

XX PD 17-JUN-1999.

XX PF 10-DEC-1998; 98WO-AU01023.

PR 04-AUG-1998; 98AU-0005028.

PR 10-DEC-1997; 97AU-0000839.

PR 31-DEC-1997; 97AU-0001182.

PR 30-JAN-1998; 98AU-0001546.

PR 10-MAR-1998; 98AU-0002264.

PR 09-APR-1998; 98AU-0002911.

PR 23-APR-1998; 98AU-0003128.

PR 05-MAY-1998; 98AU-0003338.

PR 22-MAY-1998; 98AU-0003654.

PR 29-JUL-1998; 98AU-0004917.

XX PA (CSLC-) CSL LTD.

XX PI Agius CT, Barr IG, Hoaking DM, Margerets MB, Patterson MA;

XX PI Ross BC, Rothel LJ, Webb EA;

XX DR WPI; 1990-385013/32.

DR P-PSDB; Y34570.

XX PT Antigenic Porphrymonas gingivalis peptides for preventing

PT gingivitis

XX PS Claim 12; Page 268; 588PP; English.

XX CC X91536 to X91801 encode two hundred and sixty six antigenic

CC Porphrymonas gingivalis (PG) polypeptide sequences given in Y4318 to

CC Y3483. X91802 to X9189 represent PCR primers used in the isolation

CC of the PG polypeptides. The PG polypeptides have antibacterial activity

CC with a vaccine mechanism of action. The PG polypeptides can be used as

CC vaccines especially against Porphyromonas gingivalis. Probes can be

CC used to detect Porphyromonas gingivalis in standard hybridisation assays.

CC gingivitis.
 XX SQ Sequence 3525 BP; 1115 A; 738 C; 777 G; 895 T; 0 other;
 SQ Sequence 3696 BP; 1171 A; 774 C; 814 G; 937 T; 0 other;

Query Match 11.1%; Score 28.2; DB 20; Length 3525;
 Best Local Similarity 57.8%; Pred. No. 7.1; Mismatches 35; Indels 0; Gaps 0;
 Matches 48; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 88 ctctgcacttcattcgctgaggattttcgcggagagatccgaaatgtggaa 147
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1683 CTGTGGTGTGTCCTTGCCATCAGGATTTCCACGGACATACAGGATGCGAGCATA 1601

QY 148 ggcgttgggttcttccatggatgg 170
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1623 GCCTATCtGtCtAACCATAAGG 1601

RESULT 14
 X01787/c X91787 standard; DNA; 3696 BP.

AC x91787;
 XX DT 25-AUG-1999 (first entry)
 XX DE Porphyromonas gingivalis protein PG9 encoding DNA.
 XX KW Porphyromonas gingivalis; PG; periodontal disease; gingivitis;
 KW vaccine; antigenic; ds.
 OS Porphyromonas gingivalis.
 OS XX WO9929870-A1.
 PN XX PD 17-JUN-1999.
 XX PF 10-DEC-1998; 98WO-AU01023.
 XX PR 04-AUG-1998; 98AU-0005028.
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 PR 29-JUL-1998; 98AU-0004917.

PA (CSLC-) CSL LTD.
 XX PI Agius CT, Barr IG, Hocking DM, Margetts MB, Patterson MA;
 PI Ross BC, Rotheil LJ, Webb EA;
 XX DR WPI; 1999-385613/32.
 DR P-PSDB; Y34569.

PT Antigenic Porphyromonas gingivalis peptides for preventing
 PT gingivitis
 PT
 PS Claim 12; Page 266-267; 580pp; English.
 XX X91536 to X91801 encode two hundred and sixty six antigenic
 CC Porphyromonas gingivalis (PG) polypeptide sequences given in Y34318 to
 CC Y34583. X91802 to X91989 represent PCR primers used in the isolation
 CC of the PG polypeptides. The PG polypeptides have antibacterial activity
 CC with a vaccine mechanism of action. The PG polypeptides can be used as
 CC vaccines especially against Porphyromonas gingivalis. Probes can be
 CC used to detect Porphyromonas gingivalis in standard hybridisation assays.
 CC Porphyromonas gingivalis is involved in periodontal disease especially
 CC gingivitis.
 XX SQ Sequence 3798 BP; 1195 A; 792 C; 835 G; 976 T; 0 other;

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